

### **In the Specification**

Please replace the paragraph bridging pages 3 and 4 with the following paragraph:

- Figure 1 represents the Northern blot analysis, the nucleotide sequences and the deduced amino acid sequence, as well as the hydrophobicity profile and a schematic of TWIK-1. (a): expression of TWIK-1 mRNA in human tissues; each track contains 5 µg of poly(A)<sup>+</sup>; the autoradiograph was exposed for 24 hours. (b) CDNA sequence of TWIK-1 and the amino acid sequences of the coding sequence. The supposed transmembranal segments are circled and the P domains are underlined; o represents a potential glycosylation site and ■ represents the threonine residue in the consensus recognition site of protein kinase C. (c): the hydrophobicity analysis and the topology of TWIK-1 deduced from it; the hydrophobicity values were calculated according to the method of Kyte and Doolittle (window size of 11 amino acids) and are presented in relation to the position of the amino acid; the shaded hydrophobic peaks correspond to the transmembranal segments. (d): a schematic of TWIK-1, showing the configuration of the P1, P2 and M1-M4 domains.